

Class__Exercise__4__210615

2024-09-02

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed      dist
##  Min.   : 4.0    Min.   :  2.00
##  1st Qu.:12.0    1st Qu.: 26.00
##  Median :15.0    Median : 36.00
##  Mean   :15.4    Mean    : 42.98
##  3rd Qu.:19.0    3rd Qu.: 56.00
##  Max.   :25.0    Max.    :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

```
library(ggplot2)
library(lsr)
library(psych)
```

```
##
## Attaching package: 'psych'
```

```
## The following objects are masked from 'package:ggplot2':
##
##   %+%, alpha
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v lubridate  1.9.3      v tibble    3.2.1
## v purrr      1.0.2      v tidyr     1.3.1
```

```
## -- Conflicts ----- tidyverse_conflicts() --
## x psych::%+%( ) masks ggplot2::%+%( )
```

```
## x psych::alpha() masks ggplot2::alpha()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
install.packages("ggcorrplot", repos = "http://cran.us.r-project.org")
```

```
## Installing package into 'C:/Users/hp/AppData/Local/R/win-library/4.4'
## (as 'lib' is unspecified)
```

```
## package 'ggcorrplot' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
## C:\Users\hp\AppData\Local\Temp\RtmpsNfPqc\downloaded_packages
```

```
library(ggcorrplot)
```

```
#USED an unknown dataset of 79 urine specimens which were analyzed in an effort to determine if certain
physical characteristics of the urine might be related to the formation of calcium oxalate crystals. #contains
7 variables and 77 rows(dropping the rownumber var)
```

```
setwd("C:/Users/hp/Documents/GitHub/BSE658/Module 3/Notebooks/")
filed <- read.csv("urine.csv", sep = ",", header = TRUE)
filed
```

```
##      rownames r gravity   ph osmo cond urea  calc
## 1          1 0    1.021 4.91  725   NA  443  2.45
## 2          2 0    1.017 5.74  577 20.0  296  4.49
## 3          3 0    1.008 7.20  321 14.9  101  2.36
## 4          4 0    1.011 5.51  408 12.6  224  2.15
## 5          5 0    1.005 6.52  187  7.5   91  1.16
## 6          6 0    1.020 5.27  668 25.3  252  3.34
## 7          7 0    1.012 5.62  461 17.4  195  1.40
## 8          8 0    1.029 5.67 1107 35.9  550  8.48
## 9          9 0    1.015 5.41  543 21.9  170  1.16
## 10         10 0    1.021 6.13  779 25.7  382  2.21
## 11         11 0    1.011 6.19  345 11.5  152  1.93
## 12         12 0    1.025 5.53  907 28.4  448  1.27
## 13         13 0    1.006 7.12  242 11.3   64  1.03
## 14         14 0    1.007 5.35  283  9.9  147  1.47
## 15         15 0    1.011 5.21  450 17.9  161  1.53
## 16         16 0    1.018 4.90  684 26.1  284  5.09
## 17         17 0    1.007 6.63  253  8.4  133  1.05
## 18         18 0    1.025 6.81  947 32.6  395  2.03
## 19         19 0    1.008 6.88  395 26.1   95  7.68
## 20         20 0    1.014 6.14  565 23.6  214  1.45
## 21         21 0    1.024 6.30  874 29.9  380  5.16
## 22         22 0    1.019 5.47  760 33.8  199  0.81
## 23         23 0    1.014 7.38  577 30.1   87  1.32
## 24         24 0    1.020 5.96  631 11.2  422  1.55
## 25         25 0    1.023 5.68  749 29.0  239  1.52
## 26         26 0    1.017 6.76  455  8.8  270  0.77
```

## 27	27 0	1.017	7.61	527	25.8	75	2.17
## 28	28 0	1.010	6.61	225	9.8	72	0.17
## 29	29 0	1.008	5.87	241	5.1	159	0.83
## 30	30 0	1.020	5.44	781	29.0	349	3.04
## 31	31 0	1.017	7.92	680	25.3	282	1.06
## 32	32 0	1.019	5.98	579	15.5	297	3.93
## 33	33 0	1.017	6.56	559	15.8	317	5.38
## 34	34 0	1.008	5.94	256	8.1	130	3.53
## 35	35 0	1.023	5.85	970	38.0	362	4.54
## 36	36 0	1.020	5.66	702	23.6	330	3.98
## 37	37 0	1.008	6.40	341	14.6	125	1.02
## 38	38 0	1.020	6.35	704	24.5	260	3.46
## 39	39 0	1.009	6.37	325	12.2	97	1.19
## 40	40 0	1.018	6.18	694	23.3	311	5.64
## 41	41 0	1.021	5.33	815	26.0	385	2.66
## 42	42 0	1.009	5.64	386	17.7	104	1.22
## 43	43 0	1.015	6.79	541	20.9	187	2.64
## 44	44 0	1.010	5.97	343	13.4	126	2.31
## 45	45 0	1.020	5.68	876	35.8	308	4.49
## 46	46 1	1.021	5.94	774	27.9	325	6.96
## 47	47 1	1.024	5.77	698	19.5	354	13.00
## 48	48 1	1.024	5.60	866	29.5	360	5.54
## 49	49 1	1.021	5.53	775	31.2	302	6.19
## 50	50 1	1.024	5.36	853	27.6	364	7.31
## 51	51 1	1.026	5.16	822	26.0	301	14.34
## 52	52 1	1.013	5.86	531	21.4	197	4.74
## 53	53 1	1.010	6.27	371	11.2	188	2.50
## 54	54 1	1.011	7.01	443	21.4	124	1.27
## 55	55 1	1.022	6.21	NA	20.6	398	4.18
## 56	56 1	1.011	6.13	364	10.9	159	3.10
## 57	57 1	1.031	5.73	874	17.4	516	3.01
## 58	58 1	1.020	7.94	567	19.7	212	6.81
## 59	59 1	1.040	6.28	838	14.3	486	8.28
## 60	60 1	1.021	5.56	658	23.6	224	2.33
## 61	61 1	1.025	5.71	854	27.0	385	7.18
## 62	62 1	1.026	6.19	956	27.6	473	5.67
## 63	63 1	1.034	5.24	1236	27.3	620	12.68
## 64	64 1	1.033	5.58	1032	29.1	430	8.94
## 65	65 1	1.015	5.98	487	14.8	198	3.16
## 66	66 1	1.013	5.58	516	20.8	184	3.30
## 67	67 1	1.014	5.90	456	17.8	164	6.99
## 68	68 1	1.012	6.75	251	5.1	141	0.65
## 69	69 1	1.025	6.90	945	33.6	396	4.18
## 70	70 1	1.026	6.29	833	22.2	457	4.45
## 71	71 1	1.028	4.76	312	12.4	10	0.27
## 72	72 1	1.027	5.40	840	24.5	395	7.64
## 73	73 1	1.018	5.14	703	29.0	272	6.63
## 74	74 1	1.022	5.09	736	19.8	418	8.53
## 75	75 1	1.025	7.90	721	23.6	301	9.04
## 76	76 1	1.017	4.81	410	13.3	195	0.58
## 77	77 1	1.024	5.40	803	21.8	394	7.82
## 78	78 1	1.016	6.81	594	21.4	255	12.20
## 79	79 1	1.015	6.03	416	12.8	178	9.39

```

filed <- filed %>% drop_na()
filed <- subset(filed, select = c(r,gravity,ph,osmo,cond,urea,calc))
filed

```

##	r	gravity	ph	osmo	cond	urea	calc
## 1	0	1.017	5.74	577	20.0	296	4.49
## 2	0	1.008	7.20	321	14.9	101	2.36
## 3	0	1.011	5.51	408	12.6	224	2.15
## 4	0	1.005	6.52	187	7.5	91	1.16
## 5	0	1.020	5.27	668	25.3	252	3.34
## 6	0	1.012	5.62	461	17.4	195	1.40
## 7	0	1.029	5.67	1107	35.9	550	8.48
## 8	0	1.015	5.41	543	21.9	170	1.16
## 9	0	1.021	6.13	779	25.7	382	2.21
## 10	0	1.011	6.19	345	11.5	152	1.93
## 11	0	1.025	5.53	907	28.4	448	1.27
## 12	0	1.006	7.12	242	11.3	64	1.03
## 13	0	1.007	5.35	283	9.9	147	1.47
## 14	0	1.011	5.21	450	17.9	161	1.53
## 15	0	1.018	4.90	684	26.1	284	5.09
## 16	0	1.007	6.63	253	8.4	133	1.05
## 17	0	1.025	6.81	947	32.6	395	2.03
## 18	0	1.008	6.88	395	26.1	95	7.68
## 19	0	1.014	6.14	565	23.6	214	1.45
## 20	0	1.024	6.30	874	29.9	380	5.16
## 21	0	1.019	5.47	760	33.8	199	0.81
## 22	0	1.014	7.38	577	30.1	87	1.32
## 23	0	1.020	5.96	631	11.2	422	1.55
## 24	0	1.023	5.68	749	29.0	239	1.52
## 25	0	1.017	6.76	455	8.8	270	0.77
## 26	0	1.017	7.61	527	25.8	75	2.17
## 27	0	1.010	6.61	225	9.8	72	0.17
## 28	0	1.008	5.87	241	5.1	159	0.83
## 29	0	1.020	5.44	781	29.0	349	3.04
## 30	0	1.017	7.92	680	25.3	282	1.06
## 31	0	1.019	5.98	579	15.5	297	3.93
## 32	0	1.017	6.56	559	15.8	317	5.38
## 33	0	1.008	5.94	256	8.1	130	3.53
## 34	0	1.023	5.85	970	38.0	362	4.54
## 35	0	1.020	5.66	702	23.6	330	3.98
## 36	0	1.008	6.40	341	14.6	125	1.02
## 37	0	1.020	6.35	704	24.5	260	3.46
## 38	0	1.009	6.37	325	12.2	97	1.19
## 39	0	1.018	6.18	694	23.3	311	5.64
## 40	0	1.021	5.33	815	26.0	385	2.66
## 41	0	1.009	5.64	386	17.7	104	1.22
## 42	0	1.015	6.79	541	20.9	187	2.64
## 43	0	1.010	5.97	343	13.4	126	2.31
## 44	0	1.020	5.68	876	35.8	308	4.49
## 45	1	1.021	5.94	774	27.9	325	6.96
## 46	1	1.024	5.77	698	19.5	354	13.00
## 47	1	1.024	5.60	866	29.5	360	5.54
## 48	1	1.021	5.53	775	31.2	302	6.19

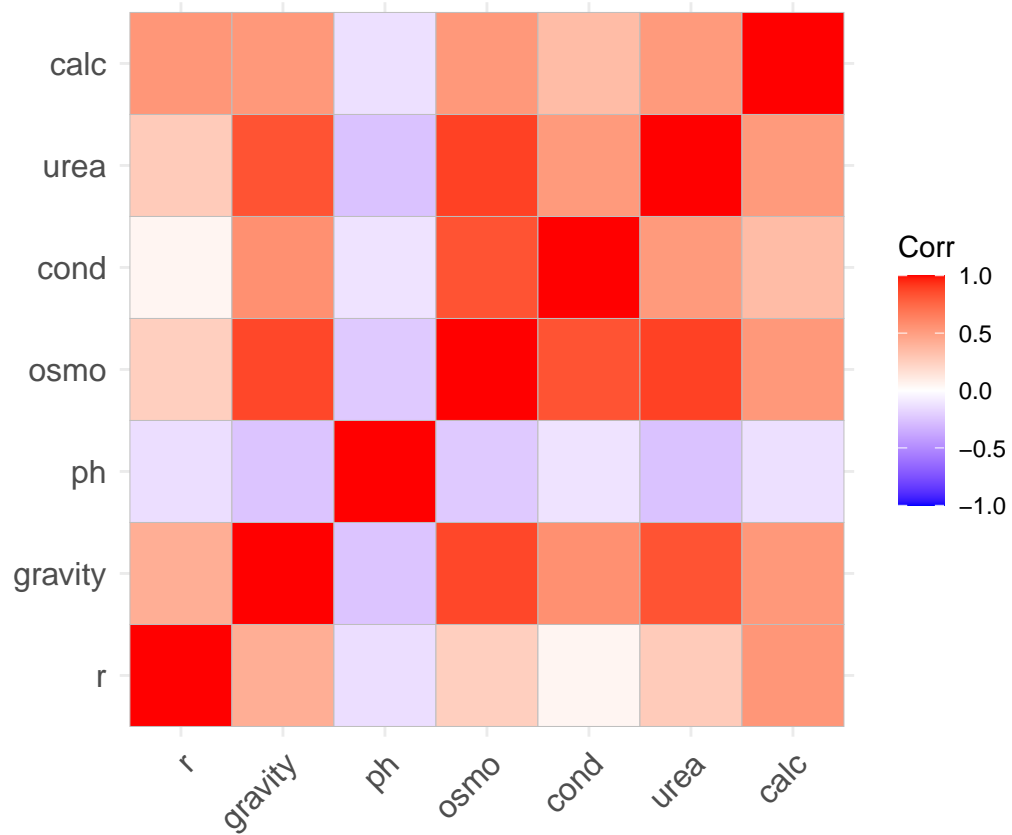
```
## 49 1 1.024 5.36 853 27.6 364 7.31
## 50 1 1.026 5.16 822 26.0 301 14.34
## 51 1 1.013 5.86 531 21.4 197 4.74
## 52 1 1.010 6.27 371 11.2 188 2.50
## 53 1 1.011 7.01 443 21.4 124 1.27
## 54 1 1.011 6.13 364 10.9 159 3.10
## 55 1 1.031 5.73 874 17.4 516 3.01
## 56 1 1.020 7.94 567 19.7 212 6.81
## 57 1 1.040 6.28 838 14.3 486 8.28
## 58 1 1.021 5.56 658 23.6 224 2.33
## 59 1 1.025 5.71 854 27.0 385 7.18
## 60 1 1.026 6.19 956 27.6 473 5.67
## 61 1 1.034 5.24 1236 27.3 620 12.68
## 62 1 1.033 5.58 1032 29.1 430 8.94
## 63 1 1.015 5.98 487 14.8 198 3.16
## 64 1 1.013 5.58 516 20.8 184 3.30
## 65 1 1.014 5.90 456 17.8 164 6.99
## 66 1 1.012 6.75 251 5.1 141 0.65
## 67 1 1.025 6.90 945 33.6 396 4.18
## 68 1 1.026 6.29 833 22.2 457 4.45
## 69 1 1.028 4.76 312 12.4 10 0.27
## 70 1 1.027 5.40 840 24.5 395 7.64
## 71 1 1.018 5.14 703 29.0 272 6.63
## 72 1 1.022 5.09 736 19.8 418 8.53
## 73 1 1.025 7.90 721 23.6 301 9.04
## 74 1 1.017 4.81 410 13.3 195 0.58
## 75 1 1.024 5.40 803 21.8 394 7.82
## 76 1 1.016 6.81 594 21.4 255 12.20
## 77 1 1.015 6.03 416 12.8 178 9.39
```

```
correlation <- cor(filed)
data.frame(correlation)
```

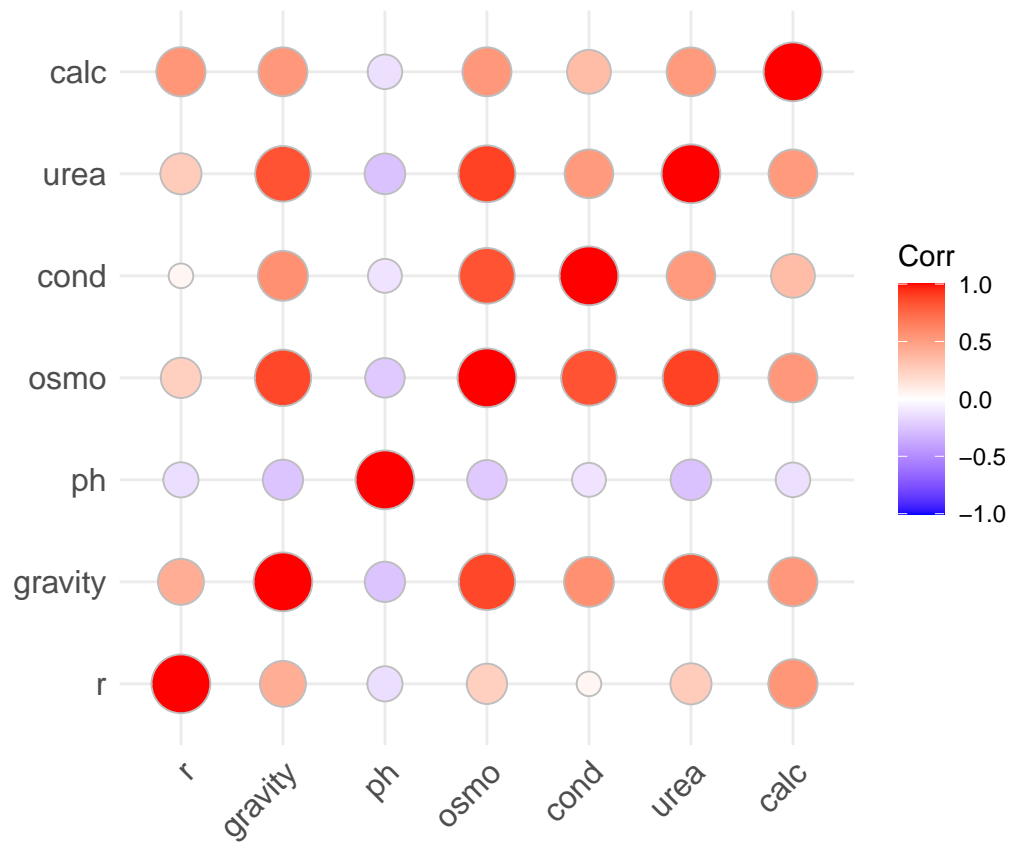
```
##          r    gravity    ph    osmo    cond    urea
## r      1.00000000 0.4231592 -0.1368720 0.2521427 0.05157744 0.2669567
## gravity 0.42315921 1.0000000 -0.2517160 0.8707383 0.56816770 0.8271763
## ph      -0.13687197 -0.2517160 1.0000000 -0.2320243 -0.11719949 -0.2605840
## osmo     0.25214275 0.8707383 -0.2320243 1.0000000 0.82556940 0.8932371
## cond     0.05157744 0.5681677 -0.1171995 0.8255694 1.00000000 0.5231409
## urea     0.26695671 0.8271763 -0.2605840 0.8932371 0.52314085 1.0000000
## calc     0.53991526 0.5308243 -0.1322306 0.5296529 0.34753125 0.5219430
##          calc
## r      0.5399153
## gravity 0.5308243
## ph      -0.1322306
## osmo     0.5296529
## cond     0.3475313
## urea     0.5219430
## calc     1.0000000
```

```
p.mat <- cor_pmat(correlation)
```

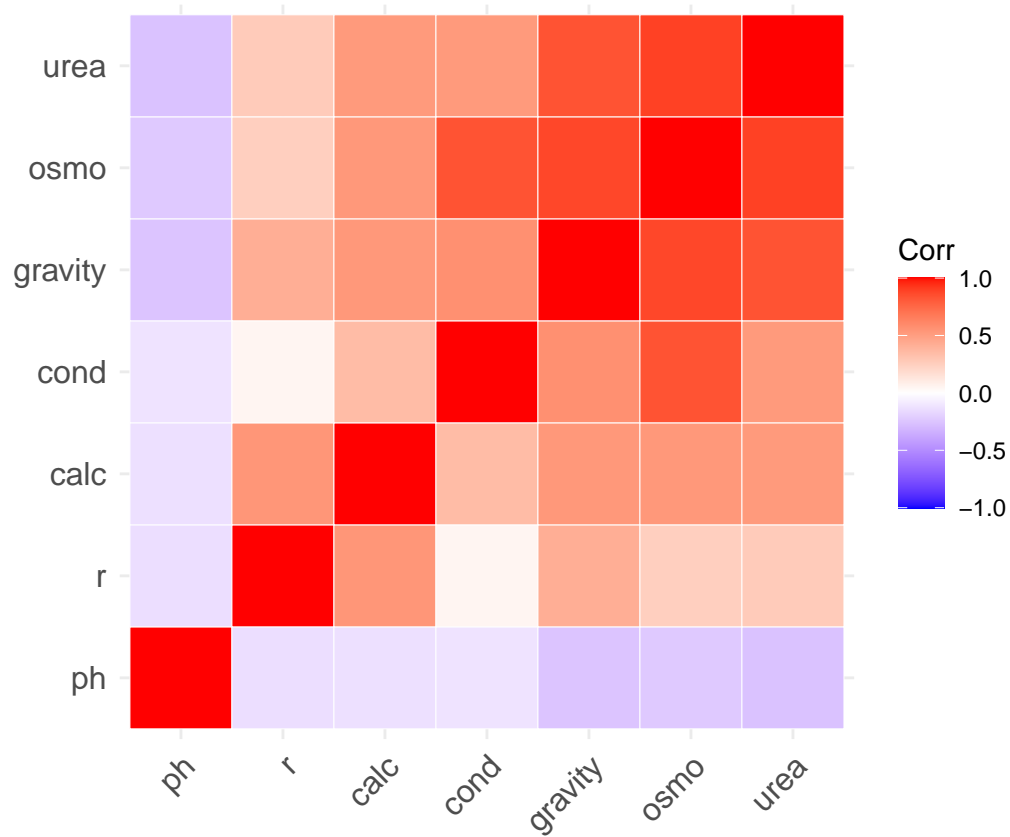
```
ggcorrplot(correlation)
```



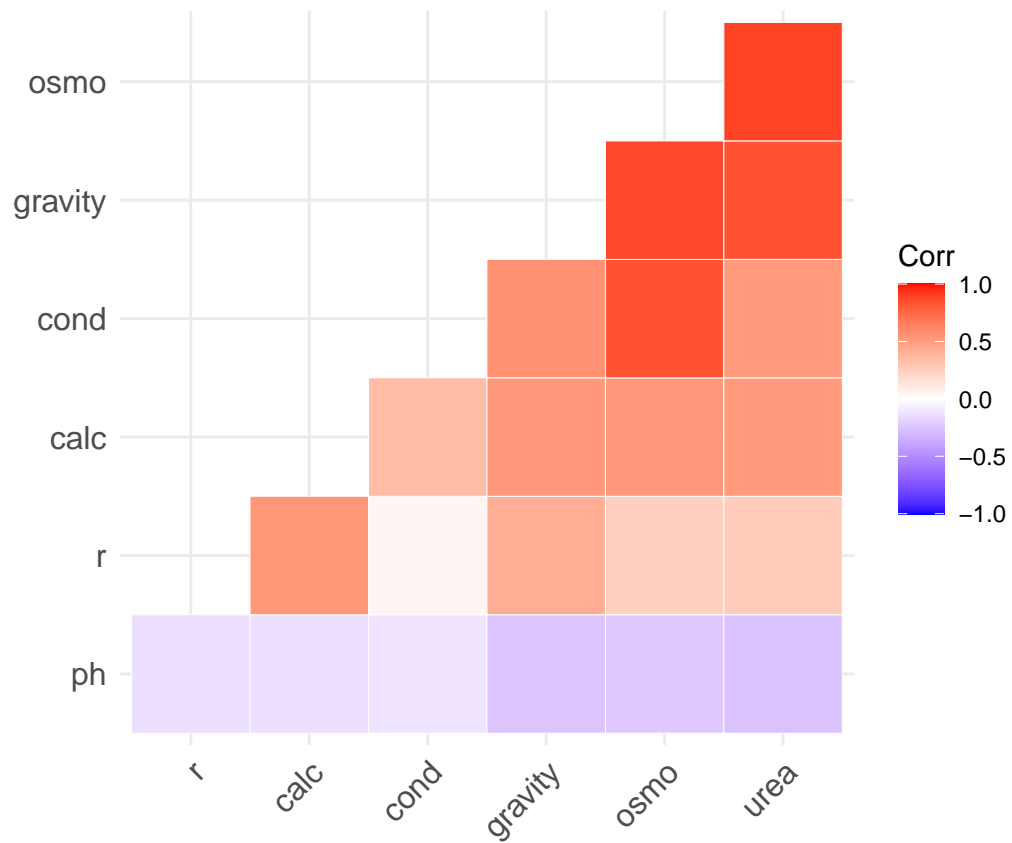
```
# method = "circle"  
ggcorrplot(correlation, method = "circle")
```



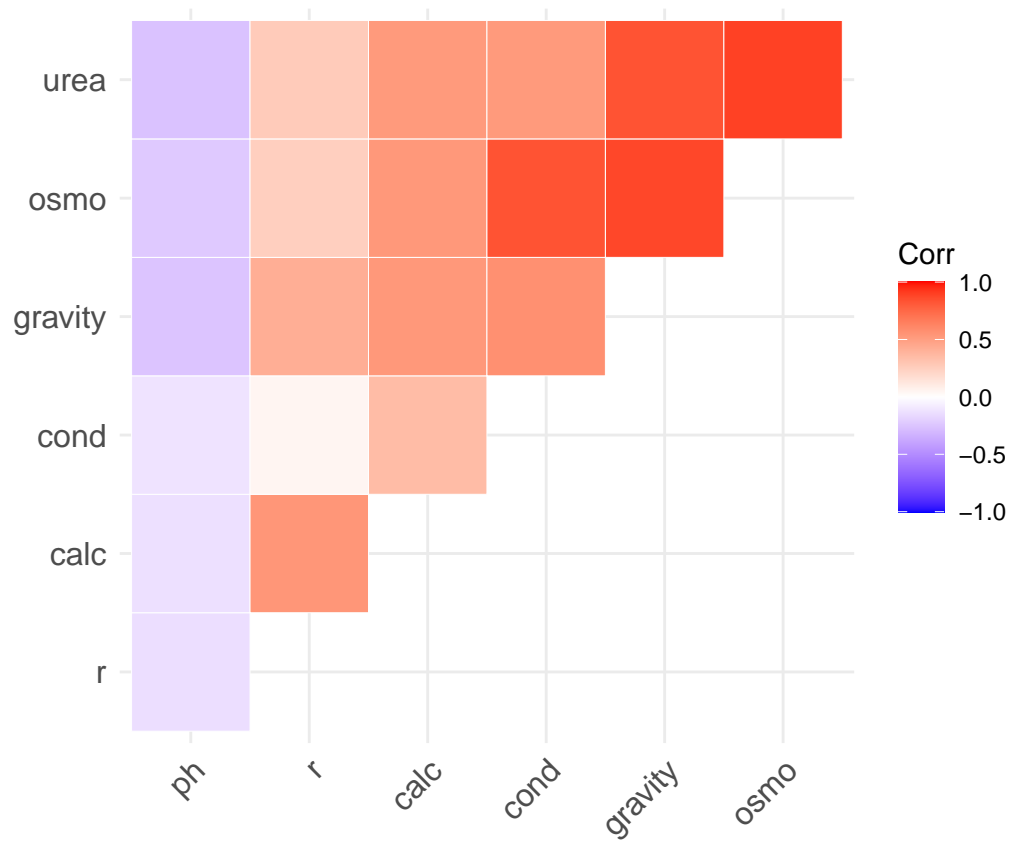
```
# Reordering the correlation matrix
# -----
# using hierarchical clustering
ggcorrplot(correlation, hc.order = TRUE, outline.col = "white")
```

```
ggcorrplot(correlation, hc.order = TRUE, type = "lower",  
  outline.col = "white")
```

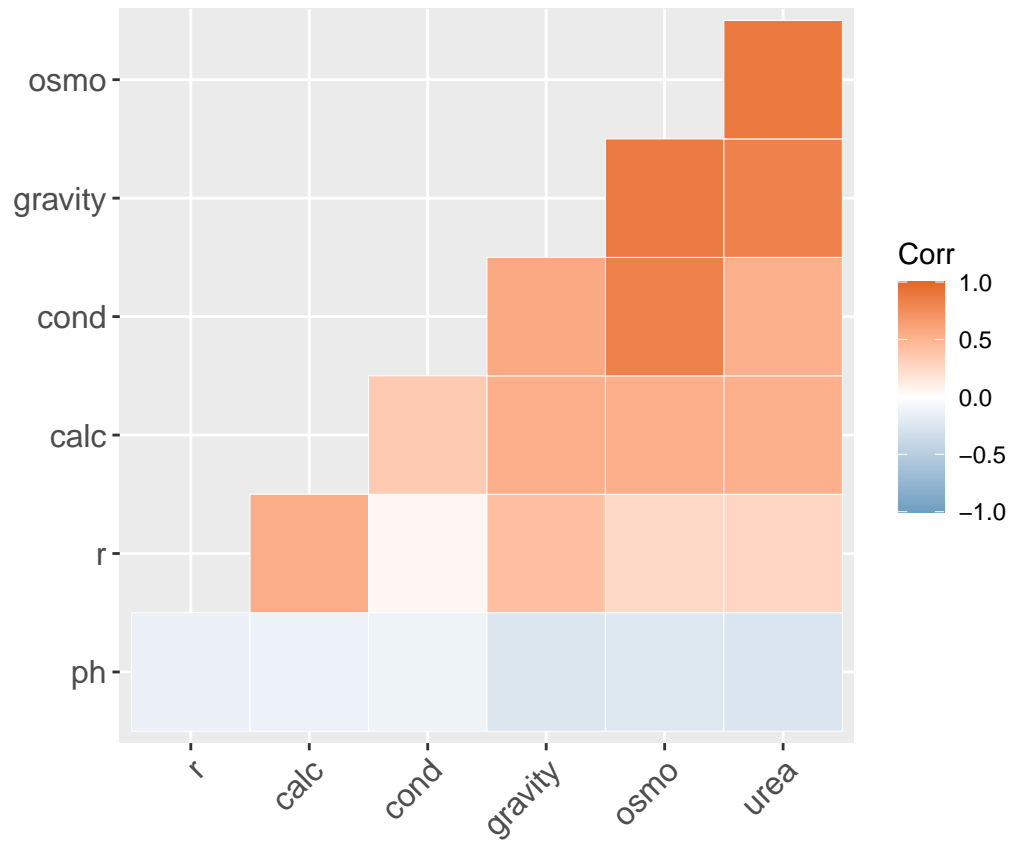


```
ggcorrplot(correlation, hc.order = TRUE, type = "upper",  
  outline.col = "white")
```



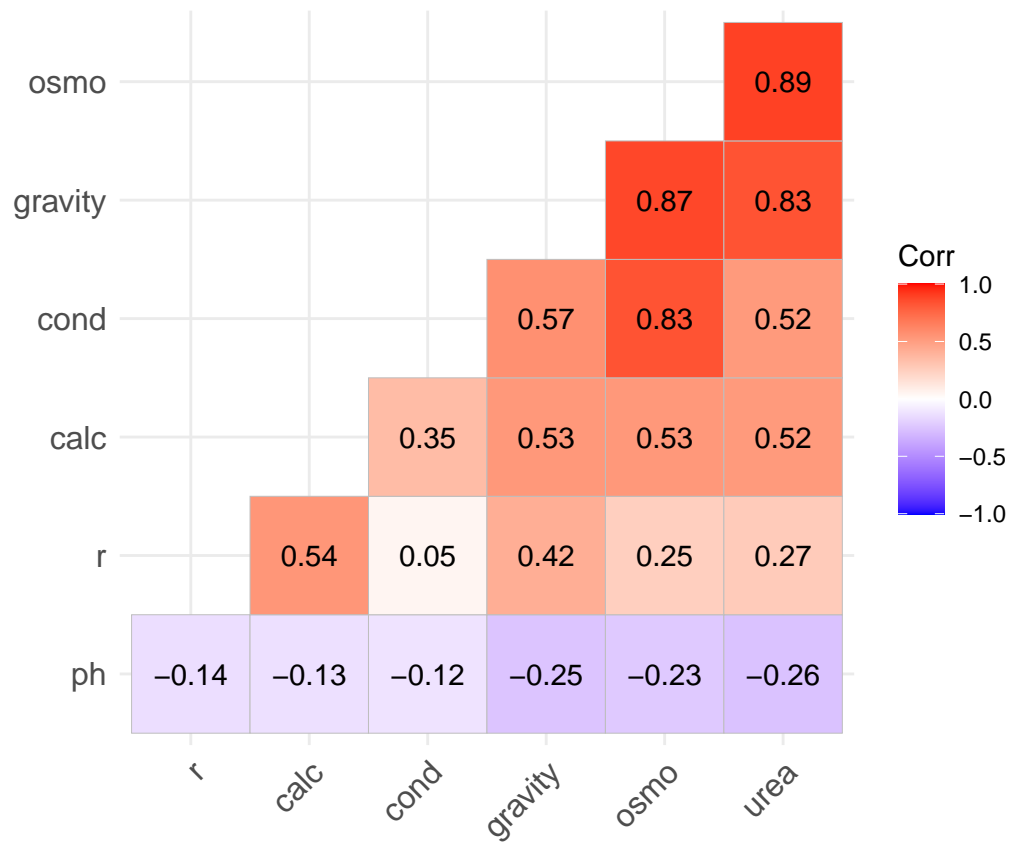
Add correlation coefficients # ————— # argument lab = TRUE

```
ggcorrplot(correlation, hc.order = TRUE, type = "lower",
  outline.col = "white",
  ggtheme = ggplot2::theme_gray,
  colors = c("#6D9EC1", "white", "#E46726"))
```



Add correlation significance level # _____ # Argument p.mat # Barring the no significant coefficient

```
ggcorrplot(correlation, hc.order = TRUE, type = "lower",
  lab = TRUE)
```



Leave blank on no significant coefficient

```
ggcorrplot(correlation, p.mat = p.mat, hc.order = TRUE,
  type = "lower", insig = "blank")
```

